

Hands On : Using MaBoSS with WebMaBoSS

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Computational Systems Biology for Complex Human Disease
from static to dynamic representations of disease mechanisms

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WebMaBoSS

A web tool for simulating Boolean models

Click [here](#) to login if you already have an account, otherwise you can quickly create one [here](#).

If you want to quickly test WebMaBoSS, you can have a look at our [demo project](#).

Model analysis

WebMaBoSS allows simulations, and multiple outputs for results. It also allows sensitivity analysis by performing single and double mutations.

Compatibility

WebMaBoSS is able to import models in MaBoSS format (bnd, cfg files), BoolNet format, SBML-qual format, or in GINsim format. It also allows to export models in any of these three formats.

Public databases


WebMaBoSS allows to browse models from CellCollective and BioModels, and import them.

WebMaBoSS was created and is maintained by the team [Computational System Biology of Cancer](#) at [Institut Curie](#).

It is open-source and available on [GitHub](#), where you can also find instructions to run it locally and tutorials.

› Create an account

Register to WebMaBoSS



Username

E-mail (optional)

Password

Confirm password

[Register](#)

> Logging in

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Demo [Sign in](#) Register

Sign in



Username

Password

Sign in

› List of projects

Projects

Name

Cell Cycle



Metastasis



Cell Fate



Tutorial



Cancer models



New project

› Creating a project

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Invasion models

Description

Models describing invasion

Close Create project

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› List of models

Models

Name

Montagud 2021 Prostate Cancer



Load model

Import model

› Loading a model

The screenshot shows the 'Load model' dialog box in the WebMaBoSS application. The background is a dimmed view of the 'Models' page, which includes a header with 'WebMaBoSS', 'Models', 'Tutorials', and 'About'. On the right of the header are 'Profile' and 'Logout' links. The main content area of the background page has a 'Models' title, a 'Name' field containing 'Montagud 2021 Prostate Cancer', and two buttons: 'Load model' and 'Import model'. The 'Load model' dialog box is centered and contains the following fields: 'Name' with the text 'Cohen 2015 Invasion model', 'Type' with a dropdown menu showing 'MaBoSS', 'BND file' with the text 'metastasis.bnd' and a 'Browse' button, and 'CFG file' with the text 'metastasis.cfg' and a 'Browse' button. At the bottom of the dialog are two buttons: a red 'Close' button and a blue 'Load model' button.

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Models

Name

Montagud 2021 Prostate Cancer

Load model Import model

Load model

Name

Cohen 2015 Invasion model

Type

MaBoSS

BND file

metastasis.bnd Browse

CFG file

metastasis.cfg Browse

Close Load model

- › Importing a model

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Import model

BioModels

CellCollective

| Name | Author |
|---|------------------------|
| Traynard2016 - Mammalian cell cycle regulation - Logical Model | Pauline Traynard |
| Cacace2020 - Logical model of the regulatory network controlling... | Denis Thieffry |
| Howell2020- Compartmental Logical model of mitotic exit | Rowan Howell |
| Terfve2012 - Signalling in liver cancer - logical model | Vijayalakshmi Chelliah |
| Floc'hlay2020 - SeaUrchin_model_ginsim | Denis Thieffry |
| Mbodj2016 - Mesoderm specification during Drosophila develop... | Denis Thieffry |
| Rodríguez-Jorge2019 - Boolean model of TCR signaling for CD4 +... | Denis Thieffry |
| Rodríguez-Jorge2019 - Boolean model of combined TCR and TLR... | Denis Thieffry |
| Afenza2018 - peripheral blood dynamics in the disease state | Szeyi Ng |

Use SBML names

Close

› Model interaction graph



› Creating a new simulation : General settings

The screenshot displays the WebMaBoSS web application interface. At the top, a navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', and user links 'Profile' and 'Logout'. A left sidebar contains a menu with 'Cohen 2015 Invasion' (selected), 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and features a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, showing the 'General' tab. The dialog contains the following fields and controls:

- Name:** A text input field with the placeholder 'Name of the simulation'.
- Max time:** A numeric input field set to 40.
- Sample count:** A numeric input field set to 1000.
- Discrete time:** A toggle switch currently turned off.
- Use physical random generator:** A toggle switch currently turned off.
- Pseudorandom seed:** A numeric input field set to 0.

At the bottom of the dialog, there is a red 'Close' button and a 'Submit' button.

› Creating a new simulation : Initial states

The screenshot displays the WebMaBoSS web application interface. At the top, there is a navigation bar with links for 'Models', 'Tutorials', and 'About'. On the left side, a sidebar menu lists 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area shows the 'Model Cohen 2015 Invasion' page, which includes a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, featuring four tabs: 'General', 'Initial states', 'Output', and 'Mutations'. The 'Initial states' tab is currently active, showing a list of biological parameters with corresponding sliders and percentage values:

| Parameter | Value (%) |
|-----------------|-----------|
| CTNNB1 | 0 % |
| CellCycleArrest | 0 % |
| DKK1 | 0 % |
| DNADamage | 50 % |
| ECMicroenv | 50 % |
| EMT | 0 % |

At the bottom of the dialog, there are 'Close' and 'Submit' buttons.

› Creating a new simulation : Output nodes

The screenshot displays the WebMaBoSS web application interface. At the top, there is a navigation bar with links for 'Models', 'Tutorials', and 'About'. On the right side of the top bar are links for 'Profile' and 'Logout'. The left sidebar contains a menu with options: 'Cohen 2015 Invasion', 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area shows the title 'Model Cohen 2015 Invasion' and a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open in the center, featuring four tabs: 'General', 'Initial states', 'Output', and 'Mutations'. The 'Output' tab is currently selected, showing a list of nodes with toggle switches: AKT1 (off), AKT2 (off), Apoptosis (on), CDH1 (off), CDH2 (off), CTNNB1 (off), and CellCycleArrest (on). At the bottom of the dialog, there are 'Close' and 'Submit' buttons.

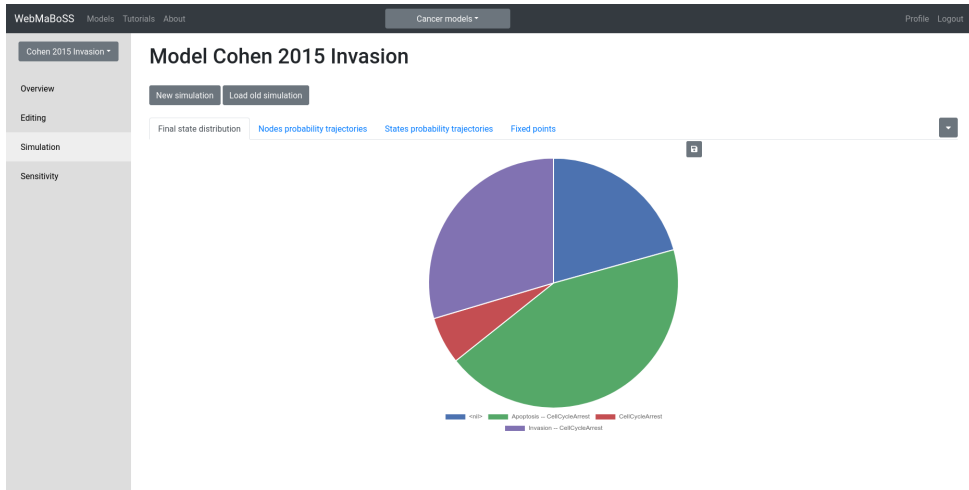
| Node | Status |
|-----------------|--------|
| AKT1 | Off |
| AKT2 | Off |
| Apoptosis | On |
| CDH1 | Off |
| CDH2 | Off |
| CTNNB1 | Off |
| CellCycleArrest | On |

› Creating a new simulation : Mutants

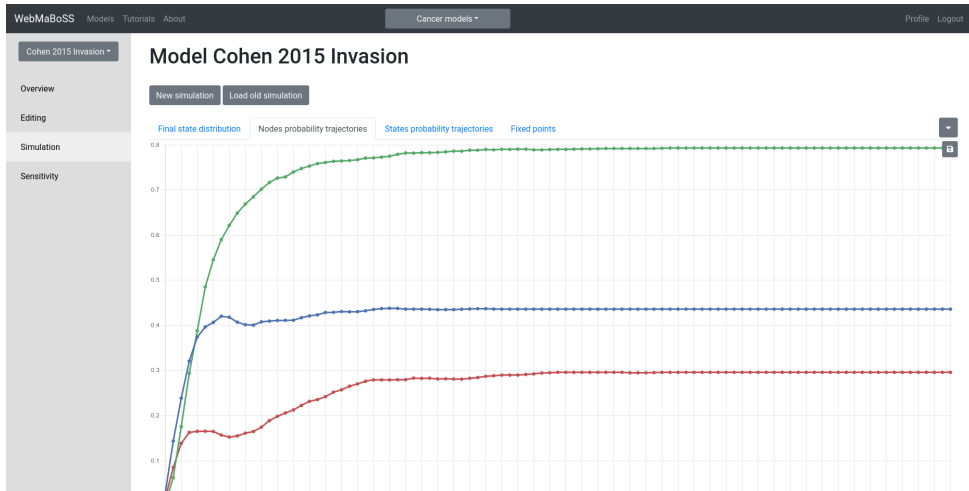
The screenshot displays the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The left sidebar contains a dropdown menu for 'Cohen 2015 Invasion' and a list of options: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area shows the title 'Model Cohen 2015 Invasion' and a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, featuring four tabs: 'General', 'Initial states', 'Output', and 'Mutations'. The 'Mutations' tab is active, showing a list of genetic elements with toggle switches: AKT1 (enabled), AKT2 (disabled), Apoptosis (disabled), CDH1 (disabled), CDH2 (disabled), CTNNB1 (disabled), and CellPulseArrest (disabled). At the bottom of the dialog are 'Close' and 'Submit' buttons.

| Element | Status |
|-----------------|----------|
| AKT1 | Enabled |
| AKT2 | Disabled |
| Apoptosis | Disabled |
| CDH1 | Disabled |
| CDH2 | Disabled |
| CTNNB1 | Disabled |
| CellPulseArrest | Disabled |

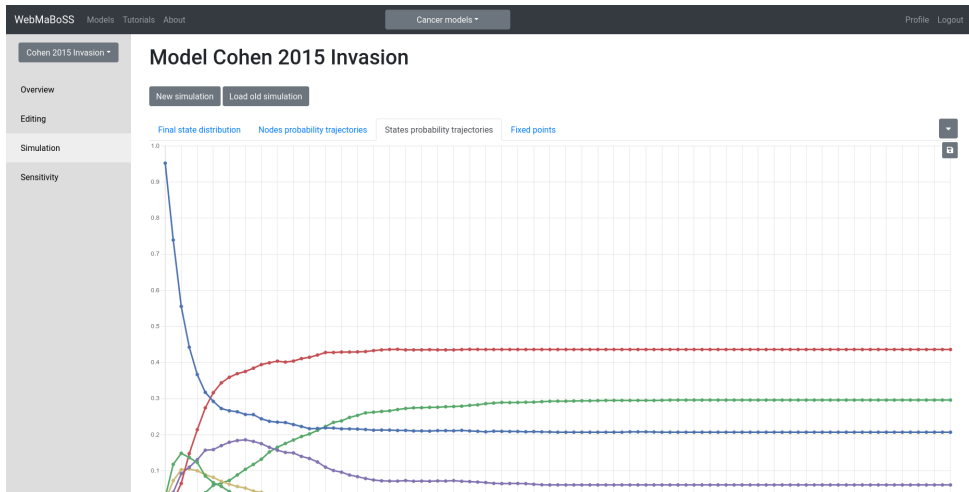
Simulation results : Final states



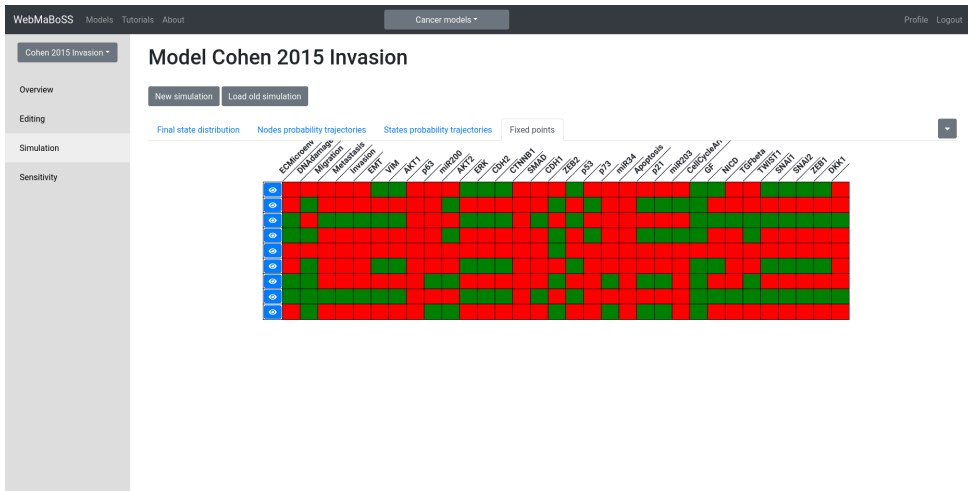
Simulation results : Node trajectories



› Simulation results : State trajectories



Simulation results : Fixed points



- Model editing : (in)activation rules

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| | | | |
|-----------------|--|--|--|
| AKT1 | | | |
| AKT2 | | | |
| Apoptosis | | | |
| CDH1 | | | |
| CDH2 | | | |
| CTNNB1 | | | |
| CellCycleArrest | | | |
| rateUp | @logic ? \$u_CellCycleArrest : 0 | | |
| rateDown | @logic ? 0 : \$d_CellCycleArrest | | |
| logic | ((p21 & IZEB2 & IAKT1 & ImlR200 & ImlR203 & miR34) (p21 & IZEB2 & IAKT1 & ImlR200 & miR203) (p21 & IZEB2 & IAKT1 & miR200) (p21 & ZEB2 & IAKT1) (p21 & IAKT1)) | | |
| DDK1 | | | |
| DNA Damage | | | |
| ECMicroenv | | | |
| EMT | | | |
| ERK | | | |
| GF | | | |
| Invasion | | | |
| Metastasis | | | |
| Migration | | | |
| NICD | | | |
| SMAD | | | |
| SNAI1 | | | |

› Model editing : (in)activation rules

The screenshot displays the WebMaBoSS web interface for editing a model. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The left sidebar shows a navigation menu with 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and features tabs for 'Rates', 'Initial values', 'Outputs', and 'Parameters'. A modal dialog box titled 'Editing formula' is open, showing a 'Name' field with 'logic' and a 'Formula' field with the expression $(!p21 \ \& \ !ZEB2 \ \& \ !AKT1 \ \& \ !miR200 \ \& \ !miR203 \ \& \ miR34) \mid (!p21$. The dialog has 'Close' and 'Submit' buttons. The background table lists various biological processes and their associated logic rules. The table has columns for the process name, the logic rule, and a set of control buttons (plus, minus, and delete icons).

| Process | Logic Rule | Controls |
|-----------------|--|----------|
| AKT1 | | Buttons |
| AKT2 | | Buttons |
| Apoptosis | | Buttons |
| CDH1 | | Buttons |
| CDH2 | | Buttons |
| CTNNB1 | | Buttons |
| CellCycleArrest | | Buttons |
| rateUp | @logic ? \$u_CellCycleArrest : 0 | Buttons |
| rateDown | @logic ? 0 : \$d_CellCycleArrest | Buttons |
| logic | $(!p21 \ \& \ !ZEB2 \ \& \ !AKT1 \ \& \ !miR200 \ \& \ !miR203 \ \& \ miR34) \mid (!p21 \ \& \ !ZEB2 \ \& \ !AKT1 \ \& \ !miR200 \ \& \ !miR203) \mid (!p21 \ \& \ !ZEB2 \ \& \ !AKT1 \ \& \ !miR200) \mid (!p21 \ \& \ !ZEB2 \ \& \ !AKT1) \mid (p21 \ \& \ !AKT1)$ | Buttons |
| DKK1 | | Buttons |
| DNA damage | | Buttons |
| ECMicroenv | | Buttons |
| EMT | | Buttons |
| ERK | | Buttons |
| GF | | Buttons |
| Invasion | | Buttons |
| Metastasis | | Buttons |
| Migration | | Buttons |
| NICD | | Buttons |
| SMAD | | Buttons |
| SNAI1 | | Buttons |

› Model editing : Initial states

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| | | |
|-----------------|-------------------------------------|-----|
| | <input checked="" type="checkbox"/> | 50% |
| AKT1 | <input type="checkbox"/> | 0% |
| AKT2 | <input type="checkbox"/> | 0% |
| Apoptosis | <input type="checkbox"/> | 0% |
| CDH1 | <input type="checkbox"/> | 0% |
| CDH2 | <input type="checkbox"/> | 0% |
| CTNNB1 | <input type="checkbox"/> | 0% |
| CellCycleArrest | <input type="checkbox"/> | 0% |
| DKK1 | <input type="checkbox"/> | 0% |
| DNA damage | <input checked="" type="checkbox"/> | 50% |
| ECMicroenv | <input checked="" type="checkbox"/> | 50% |
| EMT | <input type="checkbox"/> | 0% |
| ERK | <input type="checkbox"/> | 0% |

› Model editing : Output nodes

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| | |
|-----------------|-------------------------------------|
| | <input type="checkbox"/> |
| AKT1 | <input type="checkbox"/> |
| AKT2 | <input type="checkbox"/> |
| Apoptosis | <input checked="" type="checkbox"/> |
| CDH1 | <input type="checkbox"/> |
| CDH2 | <input type="checkbox"/> |
| CTNNB1 | <input type="checkbox"/> |
| CellCycleArrest | <input checked="" type="checkbox"/> |
| DKK1 | <input type="checkbox"/> |
| DNA damage | <input type="checkbox"/> |
| ECMicroenv | <input type="checkbox"/> |
| EMT | <input type="checkbox"/> |
| ERK | <input type="checkbox"/> |
| GF | <input type="checkbox"/> |
| Invasion | <input checked="" type="checkbox"/> |

› Model editing : Parameters

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| | | | |
|---------------------|---|---|---|
| \$d_AKT1 | 1 |  |  |
| \$d_AKT2 | 1 |  |  |
| \$d_Apoptosis | 1 |  |  |
| \$d_CDH1 | 1 |  |  |
| \$d_CDH2 | 1 |  |  |
| \$d_CTNNB1 | 1 |  |  |
| \$d_CellCycleArrest | 1 |  |  |
| \$d_DKK1 | 1 |  |  |
| \$d_DNA Damage | 1 |  |  |
| \$d_ECMicroenv | 1 |  |  |
| \$d_EMT | 1 |  |  |
| \$d_ERK | 1 |  |  |
| \$d_GF | 1 |  |  |
| \$d_Invasion | 1 |  |  |
| \$d_Metastasis | 1 |  |  |
| \$d_Migration | 1 |  |  |
| \$d_NICD | 1 |  |  |
| \$d_SMAD | 1 |  |  |
| \$d_SNAI1 | 1 |  |  |
| \$d_SNAI2 | 1 |  |  |
| \$d_TGFbeta | 1 |  |  |

› Model editing : Settings

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| | | |
|------------------------------------|-------|---|
| time_tick | 0.5 |  |
| max_time | 40 |  |
| sample_count | 1000 |  |
| discrete_time | 0 |  |
| use_physrandgen | 0 |  |
| seed_pseudorandom | 0 |  |
| display_traj | 0 |  |
| statdist_traj_count | 0 |  |
| statdist_cluster_threshold | 1 |  |
| thread_count | 6 |  |
| statdist_similarity_cache_max_size | 20000 |  |

› Sensitivity analysis : General settings

The screenshot displays the WebMaBoSS web application interface. At the top, a dark navigation bar contains the logo 'WebMaBoSS' and links for 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. A left sidebar lists navigation options: 'Cohen 2015 Invasion', 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and features a 'New sensitivity analysis' button. A modal dialog box titled 'New sensitivity analysis' is open, showing three tabs: 'General' (selected), 'Candidates', and 'Output'. The 'General' tab contains a 'Name' input field with the placeholder 'Name of the simulation', two toggle switches for 'Single mutations' and 'Double mutations' (both currently off), a 'Local' dropdown menu, a red 'Close' button, and a 'Submit' button.

› Sensitivity analysis : Mutant candidates

The screenshot displays the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', and 'Profile Logout'. The left sidebar shows a menu with 'Cohen 2015 Invasion' selected, and sub-items: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and contains a 'New sensitivity analysis' button. A modal window titled 'New sensitivity analysis' is open, featuring three tabs: 'General', 'Candidates', and 'Output'. The 'Candidates' tab is active, showing a list of biological processes with toggle switches: ERK (on), GF (on), Invasion (off), Metastasis (off), Migration (off), and NICD (on). At the bottom of the modal are 'Close' and 'Submit' buttons.

| Process | Status |
|------------|--------|
| ERK | On |
| GF | On |
| Invasion | Off |
| Metastasis | Off |
| Migration | Off |
| NICD | On |

› Sensitivity analysis : Output nodes

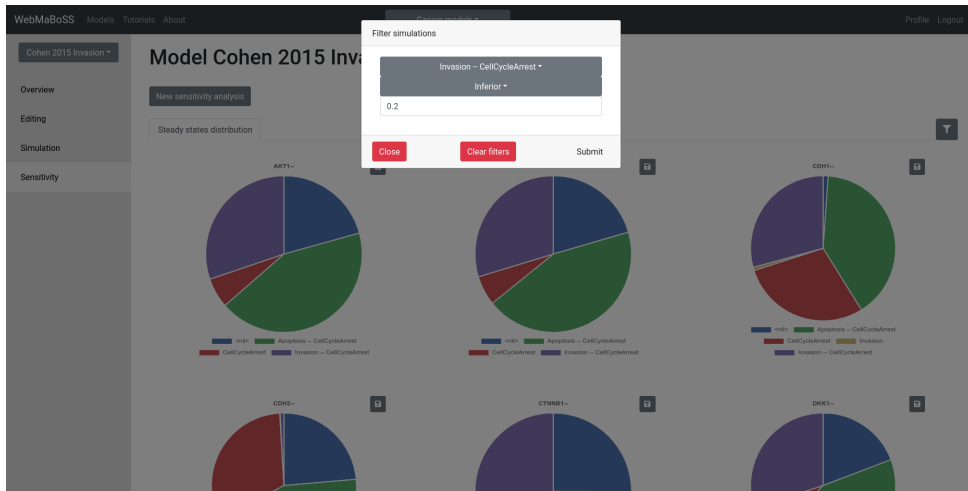
The screenshot displays the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The left sidebar shows a menu with 'Cohen 2015 Invasion' selected, and sub-items: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and contains a 'New sensitivity analysis' button. A modal dialog box titled 'New sensitivity analysis' is open, showing three tabs: 'General', 'Candidates', and 'Output'. The 'Output' tab is active, displaying a list of nodes with toggle switches: AKT1, AKT2, Apoptosis (checked), CDH1, CDH2, and CTNNB1. At the bottom of the dialog are 'Close' and 'Submit' buttons.

| Node | Toggle State |
|-----------|--------------|
| AKT1 | Off |
| AKT2 | Off |
| Apoptosis | On |
| CDH1 | Off |
| CDH2 | Off |
| CTNNB1 | Off |

› Sensitivity analysis : Results



› Sensitivity analysis : Filtering results



› Sensitivity analysis : Filtered results



- › Hands on

- › Create a new project
- › Load Cohen's model (bnd and cfg available in google drive)
- › Perform default simulation, report CellCycleArrest state final percentage
- › Perform simulation with ECMicroenv and DNADamage on, report Apoptosis node final percentage
- › Perform simulation with NICD++, p53– mutant, report number of fixed points

- › Hands on

- › Perform sensitivity analysis on single mutants, testing only inhibitions
- › Filter mutants where state Invasion – CellCycleArrest is less than 20%
- › Report mutants found with such phenotypes